NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

ASAP - Printer Rush

Applicant must file the items indicated below ~~within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a))~~.

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☒ 7. Other: *See attached error report.* _____

Applicant Must Provide:

☒ An initial or <u>substitute</u> computer readable form (CRF) copy of the "Sequence Listing".

☒ An initial or <u>substitute</u> paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

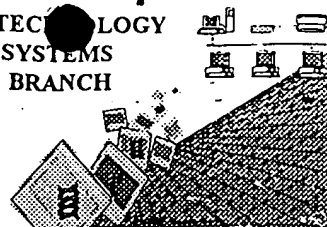For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
PatentIn Software Program Support
   Technical Assistance..............................703-287-0200
   To Purchase PatentIn Software......................703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

S. Tucker

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY SYSTEMS BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: ___O9 /328, 877C___

Source: ___16 00___

Date Processed by STIC: ___11-18-03___

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.1 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
<u>http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm</u>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. <u>Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:</u>

1. EFS-Bio (<u><http://www.uspto.gov/ebc/efs/downloads/documents.htm></u> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _09/328,877C_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
      Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
      prevent "wrapping."

2_____ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3_____ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
      Numbering   use space characters, instead.

4_____ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
      ensure your subsequent submission is saved in ASCII text.

5_____ Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules,
      each n or Xaa can only represent a single residue. Please present the maximum number of each
      residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
      "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
      previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
      the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
      Artificial or Unknown sequences.**

7_____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
      (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
      (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
      (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
      This sequence is intentionally skipped

      Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
      (NEW RULES)   <210> sequence id number
      <400> sequence id number
      000

9_✗__ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
      (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
      In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10_____ Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
      Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
      is Artificial Sequence

11_____ Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
      Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
      "Unknown." Please explain source of genetic material in <220> to <223> section.
      (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12_____ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
      "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
      listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____ Misuse of n/Xaa   "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

Does Not Comply
Corrected Diskette Needed
SEE Additional pages & back

1600

RAW SEQUENCE LISTING   DATE: 11/18/2003
PATENT APPLICATION: US/09/328,877C   TIME: 13:18:14

Input Set : A:\6142_revised.seq.txt
Output Set: N:\CRF4\11182003\I328877C.raw

```
   3 <110> APPLICANT: Gurney, Mark E.
   5        Li, Jinhe
   7        Pauley, Adele M.
   9        Pharmacia & Upjohn Company
  13 <120> TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
  15        Encode Them
  19 <130> FILE REFERENCE: 6142
C--> 23 <140> CURRENT APPLICATION NUMBER: US/09/328,877C
C--> 25 <141> CURRENT FILING DATE: 1999-06-09
E--> 29 <160> NUMBER OF SEQ ID NOS: (27)
  33 <170> SOFTWARE: PatentIn Ver. 2.0
```

Number of sequences in Sequence Listing is 32 not 27 given in <160>.

ERRORED SEQUENCES

```
  3603 <210> SEQ ID NO: (32)
  3605 <211> LENGTH: 23
  3607 <212> TYPE: DNA
  3609 <213> ORGANISM: Artificial Sequence
  3613 <220> FEATURE:
  3615 <223> OTHER INFORMATION: Description of Artificial Sequence:
  3617        Oligonucleotide primer
  3621 <400> SEQUENCE: 32
  3623 ctcagacaggtcaggacatttgg          23
E--> 3645 54.
```

remove extra material at the end of file.

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 11/18/2003
PATENT APPLICATION: US/09/328,877C   TIME: 13:18:15

Input Set : A:\6142_revised.seq.txt
Output Set: N:\CRF4\11182003\I328877C.raw

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

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Seq#:1;  Line(s)  1,3,5,7,9,11,13,15,17,19,21,23,25,27,29,31,33,35,37,39,41
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Seq#:1;  Line(s)  97,99,101,103,105,107,109,111,113,115,117,119,121,123,125
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Seq#:2;  Line(s)  185,187,203,205,207,209,211,213,215,217,219,221,223,225,227
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Seq#:6;  Line(s)  1171,1173,1175,1177,1179,1181,1183,1185,1187,1189,1191,1193
Seq#:6;  Line(s)  1195,1197,1199,1201,1203,1205,1207,1209,1211,1213,1215,1217
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 11/18/2003
PATENT APPLICATION: US/09/328,877C   TIME: 13:18:15

Input Set : **A:\6142_revised.seq.txt**
Output Set: **N:\CRF4\11182003\I328877C.raw**

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Seq#:7;  Line(s) 1371,1373,1375,1377,1379,1381,1383,1385,1387,1389,1391,1393
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VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/328,877@**

DATE: 11/18/2003
TIME: 13:18:15

Input Set : **A:\6142 revised.seq.txt**
Output Set: **N:\CRF4\11182003\I328877C.raw**

L:23 M:270 C: Current Application Number differs, Replaced Current Application Number
L:25 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:143 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:1
L:143 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:2460
M:341 Repeated in SeqNo=1
L:289 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:2
L:289 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:2460
M:341 Repeated in SeqNo=2·
L:364⊦ M:254 E: No. of Bases conflict, this line has no nucleotides.
L:29 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (27) Counted (32)

<210> 1

<211> 3550

<212> DNA

<213> Homo sapiens

<220>
<221> unsure
<222> (2485)

Numeric Identifier <223> is mandatory for 'n' and Xaa. SEE ITEM # 9 on

<220>
<221> unsure
<222> (3372)

ERROR Summary SHGET.

<400> 1

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<210> 2

<211> 3571

<212> DNA

<213> Homo sapiens


<220>
<221> unsure
<222> (2506)          See additional page 1.


<220>
<221> unsure
<222> (3393)


<400> 2
```